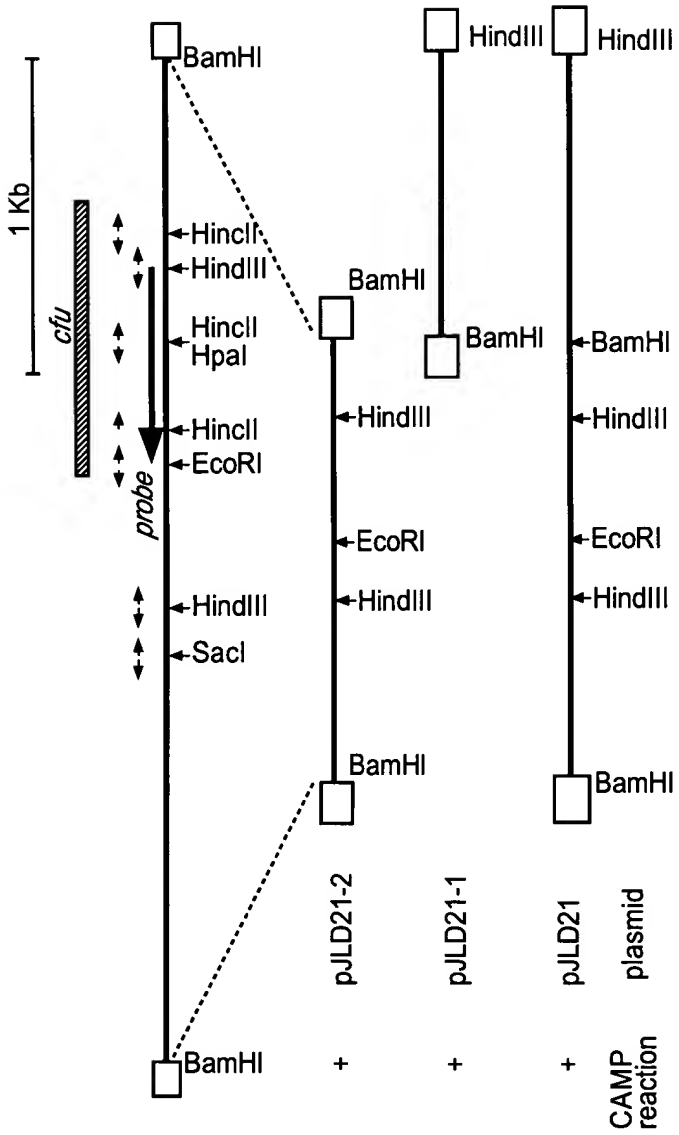

Fig. 1

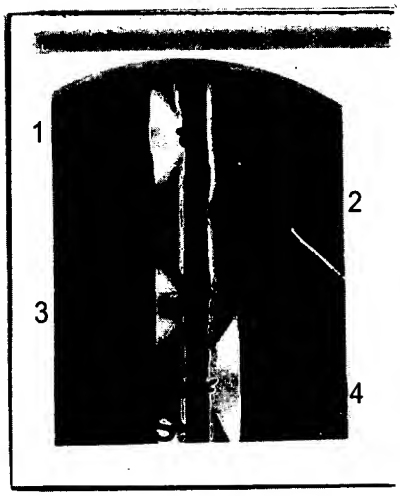

Fig. 2

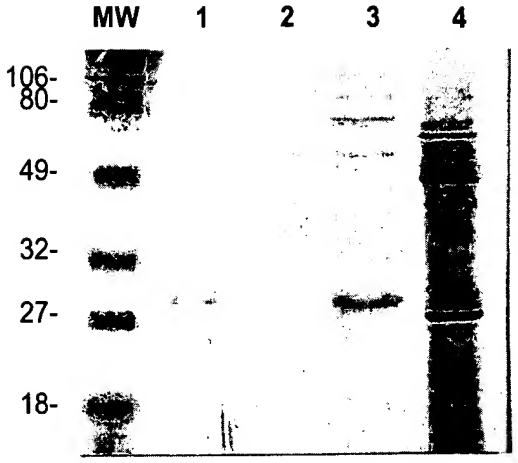

Fig. 3A

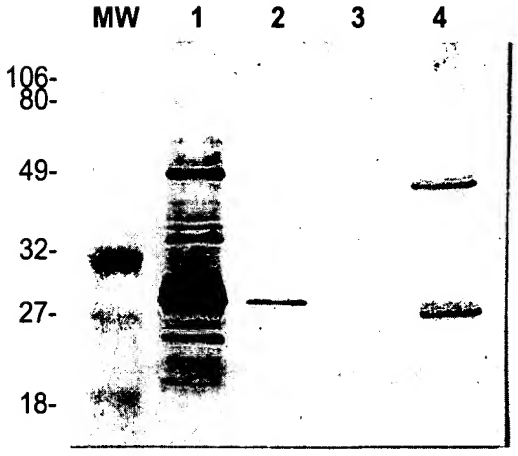

Fig. 3B

```
AATGAACATAAAATAAAAATTAATAATTATATATTTTTATGATAATCACATATATTTGAC                    60
                                                          -35

                          +1
TTAAAAAAATTGTTACTGTATGATACAGGCATAAGTACTTATTTATTTTATAGATTGCAA                   120
                    -10

TTTATAAACAATTATATTTTTCAAAGAGGAATGCTT ATG GAA TTC AAA AAG TTA CTT TAT           180
                          SD         Met Glu Phe Lys Lys Leu Leu Tyr>            8
                                        ___a____SIGNAL PEPTIDE_a___a___>

TTA ACT GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT TTA ACA AGT GTC CAA GCA  240
Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala>  28
___a___a___a___a___a___a___a____SIGNAL PEPTIDE_a___a___a___a___a___a___a___a___>

AAT CAA ATA AAT GTT AGT CAA CCA TCT AAT AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA  300
Asn Gln Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys>  48
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

GAA GAA ATT GAT AAT AGT CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT  360
Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp>  68
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

GTT AAA GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA AAT TTA  420
Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu>  88
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>
```

Fig. 4A

```
AAA ACT TCA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA AAT TCG ATT GGA ACA AGA    480
Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg>   108
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

GTA GAA GCA ATC TCT GAC GTG ATT CAA GCA ATT GTT TTT TCA ACG CAA CAG TTA ACA AAT    540
Val Glu Ala Ile Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn>   128
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

AAA GTT GAT CAA GCT CAC ATT GAT ATG GGA TTT GCT ATT ACG AAA TTA CTT ATT CGC ATT    600
Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile>   148
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

GCA GAC CCA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA CAA GTG    660
Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys Gln Val>   168
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

CAA GCG ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT AGA GCA ACT ATT TAC GTT    720
Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val>   188
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

AAA TCA AAA TTA GAC AAG CTT ATT TGG CAA ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT    780
Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu>   208
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

AAT GTA AAG AGT TTT GAA GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT    840
Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly>   228
___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>
```

Fig. 4B

```
GTA CAA TTA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG CTA CAA    900
Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val Leu Gln>   248
___b___b___b___b___b___b___b___b____MATURE PEPTIDE_b___b___b___b___b___b___b___b___>

GAA GCA TTA AAT ACT GCT CTA CAG TAAGGTAGAGATTGAATTGACGTATTAAAAAGGACT               960
Glu Ala Leu Asn Thr Ala Leu Gln>                                                   256
___b____MATURE PEPTIDE_b___b___>

GGAATTTATTAATTTCAGTCCTTTAGAATTTTTATTTAGCTGATTTACTTGTTGAAGAGA                      1020

TTTGGTGGAAAATCAAGTACCATACTTCATTTCTCCTCCAAATACTTGTATGTCGATTCC                      1080

CTTCTAAAACATAGCTAATTAGTTTAGTTTTCTGGCTAATAGATTGTACATGAAATTGTT                      1140

CAAAATTACTAGGGTAAAAGGTTTTTCTTTTTATAAATTCATCATGACTAT                               1190
```

Fig.4C

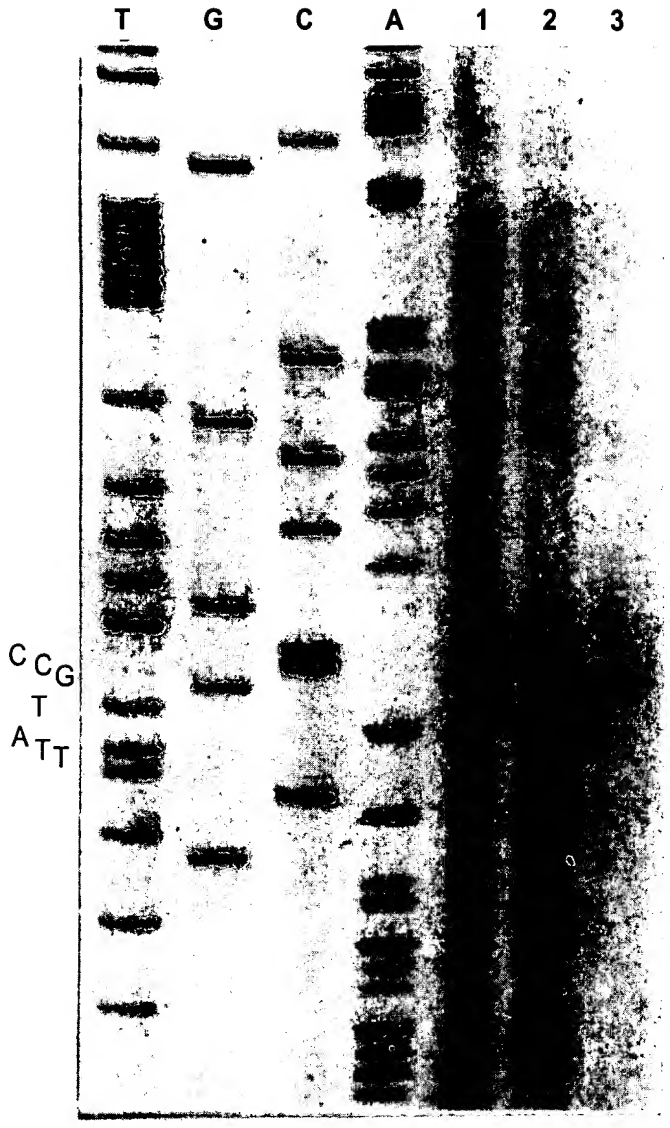

Fig. 5

```
SUCAMP    - MEFKKLLYLTGSIAGITLFSPILTSVQANQINVSQP-----SNNESNVIS -45
                                          :.   :      ::: .. ..
SAGCAMP   -                               DQVTTPQVVNHVNSNNQAQQMA -22

SUCAMP    - QKKEEIDNSLNQESAQLYALKEDVKGTEKEQSVNSAISAVENLKTSLRAN -95
              ::         :.: ::  .:. : ::. :  :: ::..:: ::::::::
SAGCAMP   - QKL-------DQDSIQLRNIKDNVQGTDYEKPVNEAITSVEKLKTSLRAN -65

SUCAMP    - PETIYDLNSIGTRVEAISDVIQAIVFSTQQLTNKVDQAHIDMGFAITKLL -145
              ::.::::::::.::::..::: :: :::: :.::: :: ::::: ::::.
SAGCAMP   - SETVYDLNSIGSRVEALTDVIEAITFSTQHLANKVSQANIDMGFGITKLV -115

SUCAMP    - IRIADPFASNESIKGQVEAVKQVQATVLTYPDLQPTDRATIYVKSKLDKL -195
              ::: ::::: .::: ::  :: .   ::::::: :::::::: ::::::
SAGCAMP   - IRILDPFASVDSIKAQVNDVKALEQKVLTYPDLKPTDRATIYTKSKLDKE -165

SUCAMP    - IWQTRITRDQKVLNVKSFEVYHQLNKAITHAVGVQLNPTVTVAQVDQEIK -245
              ::.:: ::: :::::: : ::  :::::::::::::::: ::: ::::::
SAGCAMP   - IWNTRFTRDKKVLNVKEFKVYNTLNKAITHAVGVQLNPNVTVQQVDQEIV -215

SUCAMP    - VLQEALNTALQ -256
              :: ::.:::
SAGCAMP   - TLQAALQTALK -226
```

Fig. 6

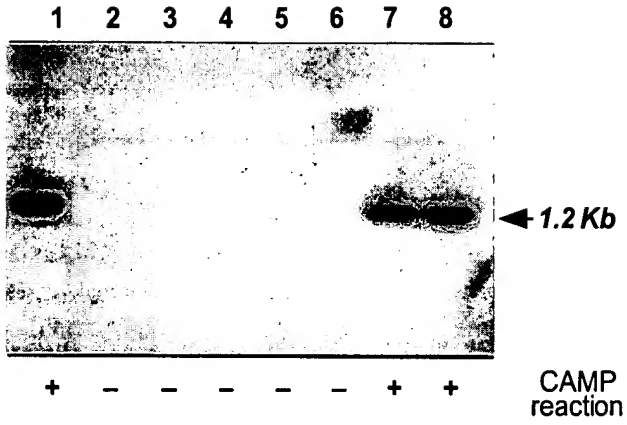

Fig. 7

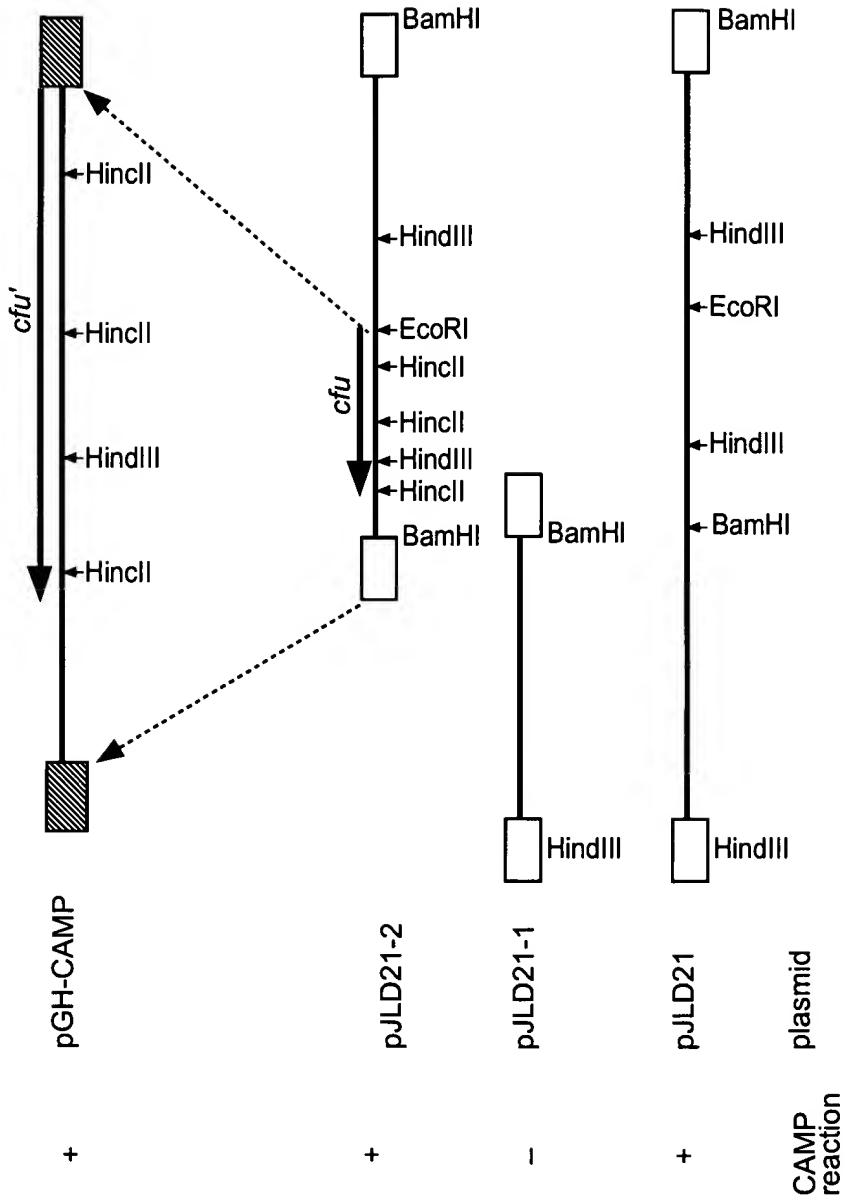

Fig. 8